

SEQUENCE LISTING

<110> Young, Karen K. Y.

<120> Compositions and Methods for Detecting Certain Flaviviruses, Including Members of the Japanese Encephalitis Virus Serogroup

<130> 022101-000230US

<140> US 10/815,480  
<141> 2004-03-31

<150> US 60/459,491  
<151> 2003-03-31

<150> US 60/552,454  
<151> 2004-03-12

<150> US 60/555,530  
<151> 2004-03-22

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      virus serogroup, KY1129

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nucleic acid	
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virus		
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<223> probe for detecting Dengue virus		
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<212> DNA		
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leukencephalitis virus		
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<210> 27
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<220>
<223> probe for detecting Modoc virus

<400> 27
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<210> 28
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<220>
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<400> 28
ggactagagg ttagaggaga ccccgccg 28

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<223> 3' untranslated region of the genome of St. Louis
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tcaaagccaa tctggccgag tgcaaagccc ctcattccga ctggggaggg tccttagcac 120
gtaggctgga gaggacgcaa aagtcatgacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgcaac 300
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<212> DNA
<213> St. Louis encephalitis virus

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tcaaagccaa tctggccgag tgcaaagccc ctcattccga ctggggaggg tccttagcac 120
gtaggctgga gaggacgcaa aagtcatgacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
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gtaggctgga gaggacgcaa aagttagacc agaaatgcca cctgaaaagca tgctaaaggt 180  
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgcaac 300  
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<210> 32  
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<220>  
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gtaggctgga gaggacgcaa aagttagacc agaaatgcca cctgaaaagca tgctaaaggt 180  
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
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<210> 33  
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gtaggctgga gaggacgcac aagttagacc agaaatgcca cctgaaaagca tgctaaaggt 180  
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaac 300  
tcggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag agtttagagg 360  
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encephalitis virus (SLEV) isolate TNM771K

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gtaggctgga gaggacgcac aagttagacc agaaatgcca cctgaaagca tgctaaaggt 180  
gctgtctgta catgccccag gaggactggg ttaacaaaagc ttaacagccc cagcggccca 240  
aaccatggag agcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaac 300  
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gtaggctgga gaggacgcac aagttagacc agaaatgcca cctgaaagca tgctaaaggt 180  
gctgtctgta catgccccag gaggactggg ttaacaaaagc ttaacagccc cagcggccca 240  
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaac 300  
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tggagaggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180  
tgtacatgcc ccaggaggac tgggttaaca aagcttaaca gcccacggg cccaaaccat 240  
ggagtgcgtg accatggcgta aaggactaga gtttagagga gaccccgctg taacttggca 300  
aggcccaaacc ccgctcaaag ctgttagagac gggggaaaggc ctagaggtt gaggagacc 360  
cttggccgtta acgcaaacaa cagcatattg acacctggaa agaca 405

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encephalitis virus (SLEV) isolate CoaV608

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gaaagcatgc taaagggtct gtctgtacat gccccaggag gactgggtta acaaagctta 180  
acagccccag cggcccaa ac catggagtgc gtgaccatgg cgtaaggact agaggttaga 240  
ggagaccccg ctgtaacttg gcaaggccca aaccgctca aagctgtaga gacggggaa 300  
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gaaagacagg agatc 375

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encephalitis virus (SLEV) isolate TBH-28

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gctgtctgtat catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240  
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaat 300  
ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag agtttagagg 360  
agacccttg ccgtaacgc aaacaacagc atattgacac ctggaaagac a 411

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encephalitis virus (SLEV) isolate VR1265

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ccaatctggc tgggtcaaaa gcccctcatt ccgactcggg agggtccctg gcacgttaggc 120  
tggagcggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180  
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gaaagcatgc taaaggtgct gtctgtacat gccccaggag gactgggtta acaaagctta 180
acagccccag cggccaaac catggagtgc gtgaccatgg cgtaaggact agaggttaga 240
ggagaccccg ctgcaacttg gcaaggccca aaccgctcg aagctgtaga gacgggggaa 300
ggactagagg ttagaggaga ccccttgccg ttaacgcaaa caacagcata ttgacacactg 360
gaaagacagg agat 374

<210> 41
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27

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<223> n = methyl-dA

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27

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27

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<220>
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<223> n = methyl-dA

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gagcccccgtc caaggacgtt aaaagnn

<210> 50
<211> 24
<212> DNA
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<220>
<223> Dengue virus type IV upstream primer

<400> 50
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<210> 51
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<210> 52
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24

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<210> 53
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<220>
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gatctctggc ctttcccagc gtcaa

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<220>
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<222> (25)...(25)
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25

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<220>	
<221> modified_base	
<222> (27)...(27)	
<223> n = methyl-dA	
<220>	
<221> modified_base	
<222> (28)...(28)	
<223> n = t-butyl-benzyl-dA	
<400> 58	
aaccggata aaaactacgg gtggagnn	28
<210> 59	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> yellow fever virus upstream primer	
<400> 59	
ataaaaaacta cgggtggaga accgga	26

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<210> 60
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> yellow fever virus upstream primer

<220>
<221> modified_base
<222> (26)...(26)
<223> n = t-butyl-benzyl-dA

<400> 60
ataaaaaacta cgggtggaga accggn                                26

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> yellow fever virus downstream primer

<400> 61
actccggtct ttccctggcg tcaa                                    24

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> yellow fever virus downstream primer

<220>
<221> modified_base
<222> (24)...(24)
<223> n = t-butyl-benzyl-dA

<400> 62
actccggtct ttccctggcg tcan                                  24

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> yellow fever virus downstream primer

<220>
<221> modified_base
<222> (23)...(23)
<223> n = methyl-dA

<220>
<221> modified_base
<222> (24)...(24)
<223> n = t-butyl-benzyl-dA

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<400> 63	
actccggct ttccctggcg tcnn	24
<210> 64	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> St Louis encephalitis virus upstream primer	
<400> 64	
caaagccccct cattccgact cgggta	25
<210> 65	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> St Louis encephalitis virus upstream primer	
<220>	
<221> modified_base	
<222> (25)...(25)	
<223> n = t-butyl-benzyl-dA	
<400> 65	
caaagccccct cattccgact cggn	25
<210> 66	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> St Louis encephalitis virus downstream primer	
<400> 66	
tctcctgtct ttccaggtgt caa	23
<210> 67	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> St Louis encephalitis virus downstream primer	
<220>	
<221> modified_base	
<222> (23)...(23)	
<223> n = t-butyl-benzyl-dA	
<400> 67	
tctcctgtct ttccaggtgt can	23
<210> 68	
<211> 23	
<212> DNA	
<213> Artificial Sequence	

<220>  
 <223> St. Louis encephalitis virus (SLEV) first primer  
 complement

<400> 68  
 ttgacacacctg gaaagacagg aga

23

<210> 69  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> St. Louis encephalitis virus (SLEV) second primer

<400> 69  
 caaagccctt cattccgact cggg

24

<210> 70  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> flavivirus anti-sense probe

<400> 70  
 gggcttcctc taacctctag tccttccccc

30

<210> 71  
 <211> 98  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF196835 region of  
 conserved sequence in 3' untranslated region

<400> 71  
 caacccagg aggactgggt gaacaaagcc gcgaagtgtat ccatgtaagc cctcagaacc 60  
 gtctcgaaag gaggacccca catgttgtaa cttcaaag

98

<210> 72  
 <211> 105  
 <212> DNA  
 <213> West Nile virus

<220>  
 <223> West Nile virus strain AF196835 region of  
 conserved sequence in 3' untranslated region

<400> 72  
 tgactgaagc ttaggtcag ggaaaggact agaggtagt ggagaccccg tgccacaaaa 60  
 caccacaaca aaacacgcata ttgacacacctg ggatagacta ggaga

105

<210> 73  
 <211> 121  
 <212> DNA  
 <213> West Nile virus

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<220>
<223> West Nile virus strain AF196835 region of
      conserved sequence in 3' untranslated region

<400> 73
cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60
gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccgggtt gccacaaaaac 120
a                                         121

<210> 74
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Example Primer 2, Japanese encephalitis virus
      serogroup amplification primer

<400> 74
tctcctagtc tatcccaagg gtcaa                                         25

<210> 75
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> detectably-labeled oligonucleotide

<220>
<221> modified_base
<222> (1)...(1)
<223> n = g attached to 3' of deoxyribose phosphate backbone
      modified by 6-carboxyfluorescein (FAM) (I) attached to 3'
      of oligonucleotide 5'GGTCTAGA3', where 5' G is modified by
      Cy5 quencher (F)

<400> 75
ngtttagaggaa gaccctccag                                         20

<210> 76
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> fluorescent moiety-quencher moiety pair in probe
      variant of SEQ ID NO:28

<220>
<221> modified_base
<222> (1)...(1)
<223> n = g attached to 3' of deoxyribose phosphate backbone
      modified by 6-carboxyfluorescein (FAM) (I) attached to 3'
      of oligonucleotide 5'GGACTAGA3', where 5' G is modified by
      Cy5 quencher (F)

<220>
<221> modified_base
<222> (20)...(20)
<223> n = phosphorylated g

```

```

<400> 76
ngttagagga gaccccgcn                                     20

<210> 77
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> fluorescent moiety-quencher moiety pair in probe
      variant of SEQ ID NO:28

<220>
<221> modified_base
<222> (1)...(1)
<223> n = g attached to 3' of deoxyribose phosphate backbone
      modified by 6-carboxyfluorescein (FAM) (I) attached to 3'
      of oligonucleotide 5'GGA-5-methyl-dC-propynyl-dU-AGA3',
      where 5' G is modified by Cy5 quencher (F)

<220>
<221> modified_base
<222> (3)...(4)
<223> n = propynyl-dU

<220>
<221> modified_base
<222> (13)...(18)
<223> n = 5-methyl-dC

<220>
<221> modified_base
<222> (20)...(20)
<223> n = phosphorylated g

<400> 77
ngnnagagga gannnngn                                     20

<210> 78
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> fluorescent moiety-quencher moiety pair in probe
      variant of SEQ ID NO:70

<220>
<221> modified_base
<222> (1)...(1)
<223> n = t attached to 3' of deoxyribose phosphate backbone
      modified by 6-carboxyfluorescein (FAM) (I) attached to 3'
      of oligonucleotide 5'GGGTCTCC3', where 5' G is modified by
      Cy5 quencher (F)

<220>
<221> modified_base
<222> (22)...(22)
<223> n = phosphorylated c

```

```

<400> 78
nctaacctct agtccttccc cn                                22

<210> 79
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> fluorescent moiety-quencher moiety pair in probe
      variant of SEQ ID NO:70

<220>
<221> modified_base
<222> (1)...(1)
<223> n = propynyl-dU attached to 3' of deoxyribose phosphate backbone
      modified by 6-carboxyfluorescein (FAM) (I) attached to 3' of
      oligonucleotide 5'GGG-propynyl-dU-5-methyl-dC-propynyl-dU-5-methyl-
      dC-5-methyl-dC3', where 5' G is modified by Cy5 quencher (F)

<220>
<221> modified_base
<222> (2)...(2)
<223> n = 5-methyl-dC

<220>
<221> modified_base
<222> (3)...(3)
<223> n = propynyl-dU

<220>
<221> modified_base
<222> (22)...(22)
<223> n = phosphorylated c

<400> 79
nnnaacctct agtccttccc cn                                22

<210> 80
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> fluorescent moiety-quencher moiety pair in probe
      variant of SEQ ID NO:25

<220>
<221> modified_base
<222> (1)...(1)
<223> n = g attached to 3' of deoxyribose phosphate backbone
      modified by 6-carboxyfluorescein (FAM) (I) attached to 3'
      of oligonucleotide 5'GGTCTAGA3', where 5' G is modified by
      Cy5 quencher (F)

<220>
<221> modified_base
<222> (20)...(20)
<223> n = phosphorylated g

```

<400> 80  
ngtttagagga gaccctccan 20

<210> 81  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF260968 region of  
conserved sequence in 3' untranslated region

<400> 81  
caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 82  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF260969 region of  
conserved sequence in 3' untranslated region

<400> 82  
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 83  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF481864 region of  
conserved sequence in 3' untranslated region

<400> 83  
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 84  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain M12294 region of  
conserved sequence in 3' untranslated region

<400> 84  
caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60  
gtctcggaag gaggacccca cgtgcttag cctcaaag 98

<210> 85  
<211> 98  
<212> DNA  
<213> West Nile virus

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<220>
<223> West Nile virus strain AF206518 region of
      conserved sequence in 3' untranslated region

<400> 85
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaaag                      98

<210> 86
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF317203 region of
      conserved sequence in 3' untranslated region

<400> 86
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaaag                      98

<210> 87
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF202541 region of
      conserved sequence in 3' untranslated region

<400> 87
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaaag                      98

<210> 88
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404757 region of
      conserved sequence in 3' untranslated region

<400> 88
caaccccagg aggactgggt gaacaaagcc gtgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaaag                      98

<210> 89
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404753 region of
      conserved sequence in 3' untranslated region

<400> 89
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaaag                      98

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<210> 90  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF404754 region of  
conserved sequence in 3' untranslated region

<400> 90  
caaccccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 91  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF404755 region of  
conserved sequence in 3' untranslated region

<400> 91  
caaccccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 92  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF404756 region of  
conserved sequence in 3' untranslated region

<400> 92  
caaccccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 93  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF017254 region of  
conserved sequence in 3' untranslated region

<400> 93  
caaccccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 94  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain L48977 region of  
conserved sequence in 3' untranslated region

<400> 94  
caaccccagg aggactgggt gaccaaagct gcgaggtat ccacgtaagc cctcagaacc 60  
gtctcggaag caggacccca cgtgctttag cctcaaag 98

<210> 95  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF196536 region of  
conserved sequence in 3' untranslated region

<400> 95  
caaccccagg aggactgggt gaacaaagcc gcgaagtat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa ctcaaag 98

<210> 96  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF196537 region of  
conserved sequence in 3' untranslated region

<400> 96  
caaccccagg aggactgggt gaacaaagct gcggagcgat ccatgtaagc cctcagaacc 60  
gtctcggaag taggacccca catgttgtag ctcaaag 98

<210> 97  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF196538 region of  
conserved sequence in 3' untranslated region

<400> 97  
caaccccagg aggactgggt gaacaaagct gcggagcgat ccatgtaagc cctcagaacc 60  
gtctcggaag taggacccca catgttgtag ttcaaag 98

<210> 98  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF196540 region of  
conserved sequence in 3' untranslated region

<400> 98  
caaccccagg aggactgggt gaacaaagct gcggagcgat ccatgtaagc cctcagaacc 60  
gtctcggaag taggacccca catgttgtag ttcaaag 98

<210> 99  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF196541 region of  
conserved sequence in 3' untranslated region

<400> 99  
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 100  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF196542 region of  
conserved sequence in 3' untranslated region

<400> 100  
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 101  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF196543 region of  
conserved sequence in 3' untranslated region

<400> 101  
caaccccagg aggactgggt taccaaagcc gcgaggtgat ccacgtaagc cctcagaacc 60  
gtctcgaaa gaggacccca cgtgttttag cctcaagg 98

<210> 102  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF297840 region of  
conserved sequence in 3' untranslated region

<400> 102  
caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60  
gcctcgaaa gaggacccca catgtttag cttcaagg 98

<210> 103  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458343 region of  
conserved sequence in 3' untranslated region

<400> 103  
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc ccccagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaagg 98

<210> 104  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458344 region of  
conserved sequence in 3' untranslated region

<400> 104  
caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 105  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458347 region of  
conserved sequence in 3' untranslated region

<400> 105  
caaccccagg aggactgggt gaacaaagct gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 106  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458348 region of  
conserved sequence in 3' untranslated region

<400> 106  
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 107  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458350 region of  
conserved sequence in 3' untranslated region

<400> 107  
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 108  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458352 region of  
conserved sequence in 3' untranslated region

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<400> 108
caaccccagg aggactgggt gaacaaagct gcggagcgat ccatgtaagc cctcagaacc 60
gcctcggaaag taggacccca catgtttag ttycaaag 98

<210> 109
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF458353 region of
      conserved sequence in 3' untranslated region

<400> 109
caaccccagg aggactgggt gaacaaagct gcggagcgat ccatgtaagc cctcagaacc 60
gcctcggaaag taggacccca catgtttag ttccaaag 98

<210> 110
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF458355 region of
      conserved sequence in 3' untranslated region

<400> 110
caaccccagg aggactgggt gaacaaagct gcgaagtgtat ccatgtaagc cctcagaacc 60
gcctcggaaag gaggacccca catgttgtaa ctccaaag 98

<210> 111
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF458358 region of
      conserved sequence in 3' untranslated region

<400> 111
caaccccagg aggactgggt taccaaagcc gcgagggtgat ccacgtaagc cctcagaacc 60
gcctcggaaa gaggacccca cgtgttttag cctcaagg 98

<210> 112
<211> 98
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF458360 region of
      conserved sequence in 3' untranslated region

<400> 112
caaccccagg aggactgggt gaacaaagcc gcgaagtgtat ccatgtaagc cctcagaacc 60
gcctcggaaag gaggacccca catgttgtaa ctccaaag 98

<210> 113
<211> 98
<212> DNA
<213> West Nile virus

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<220>  
<223> West Nile virus strain AF458361 region of  
conserved sequence in 3' untranslated region

<400> 113  
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60  
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 114  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF208017 region of  
conserved sequence in 3' untranslated region

<400> 114  
caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60  
gtctcggaag gaggacccca cgtgcttag cctcaaag 98

<210> 115  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF196539 region of  
conserved sequence in 3' untranslated region

<400> 115  
caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60  
gtctcggaag gaggacccca cgtgcttag cctcaaag 98

<210> 116  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF196535 region of  
conserved sequence in 3' untranslated region

<400> 116  
caaccccagg aggactgggt gaccaaagcc gcgaggtgat ccacgtaagc cctcagaacc 60  
gtctcggaag gaggacccca cgtgcttag cctcaagg 98

<210> 117  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458359 region of  
conserved sequence in 3' untranslated region

<400> 117  
caaccccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60  
gtctcggaag gaggacccca cgtgcttag cctcaaag 98

<210> 118  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458357 region of  
conserved sequence in 3' untranslated region

<400> 118  
caacccagg aggactgggt gaccaaagcc gcgaggtgat ccacgtaagc cctcagaacc 60  
gtctcggaag gaggacccca cgtgcttag cctcaaag 98

<210> 119  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458354 region of  
conserved sequence in 3' untranslated region

<400> 119  
caacccagg aggactgggt gaccaaagct gcgaggtgat ccacgtaagc cctcagaacc 60  
gtctcggaag gaggacccca cgtgcttag cctcaaag 98

<210> 120  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458349 region of  
conserved sequence in 3' untranslated region

<400> 120  
caacccagg aggactgggt gaccaaacct gcgaggtgat ccacgtaagc cctcagaacc 60  
gtctcggaag gaggacccca cgtgcttag cctcaaag 98

<210> 121  
<211> 98  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AF458345 region of  
conserved sequence in 3' untranslated region

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of conserved sequence in 3' untranslated region

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of conserved sequence in 3' untranslated region

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<210> 197  
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<220>
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<210> 198
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<210> 201
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<212> DNA
<213> Japanese encephalitis virus

<220>
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<220>  
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of conserved sequence in 3' untranslated region

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of conserved sequence in 3' untranslated region

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<210> 205  
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of conserved sequence in 3' untranslated region

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<220>  
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of conserved sequence in 3' untranslated region

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of conserved sequence in 3' untranslated region

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cgttcggaa gtcctccct ttcaccgga agttgaaag 99

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of conserved sequence in 3' untranslated region

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of conserved sequence in 3' untranslated region

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cgtttcggaa gtaggtccct ttcactgga agttgaaag 99

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<220>  
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of conserved sequence in 3' untranslated region

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<220>  
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<220>  
<223> St. Louis encephalitis virus strain 1750-Std  
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<212> DNA  
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<220>  
<223> St. Louis encephalitis virus strain TD6-4G-C  
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<212> DNA  
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<212> DNA  
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<220>  
<223> St. Louis encephalitis virus strain CoaV750  
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<220>  
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region of conserved sequence in 3' untranslated  
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<212> DNA  
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<220>  
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region of conserved sequence in 3' untranslated  
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<220>  
<223> St. Louis encephalitis virus strain Kern217  
region of conserved sequence in 3' untranslated  
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<220>
<223> St. Louis encephalitis virus strain CoaV608
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<210> 230
<211> 97
<212> DNA
<213> St. Louis encephalitis virus

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<223> St. Louis encephalitis virus strain TBH-28
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<210> 231
<211> 97
<212> DNA
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      region of conserved sequence in 3' untranslated
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actcgggagg gtcctggca cgtaggctgg agccgg 97

<210> 232
<211> 93
<212> DNA
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<223> St. Louis encephalitis virus strain CoaV353
      region of conserved sequence in 3' untranslated
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gggagggtcc ctggcacgta ggctggagag gac 93

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<220>
<223> Murray Valley encephalitis virus strain VR77
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region of conserved sequence in 3' untranslated  
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<220>  
<223> Murray Valley encephalitis virus strain M35172  
region of conserved sequence in 3' untranslated  
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<210> 236  
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<220>  
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region of conserved sequence in 3' untranslated  
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<220>  
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region of conserved sequence in 3' untranslated  
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<210> 238  
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<220>  
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 region of conserved sequence in 3' untranslated  
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<220>  
 <223> Murray Valley encephalitis virus strain L48975  
 region of conserved sequence in 3' untranslated  
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 <212> DNA  
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 region of conserved sequence in 3' untranslated  
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<210> 241  
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 <212> DNA  
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<220>  
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 sequence in 3' untranslated region

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<210> 242  
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 <212> DNA  
 <213> West Nile virus

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<220>
<223> West Nile virus strain AF260967 region of
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<210> 243
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<212> DNA
<213> West Nile virus

<220>
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      conserved sequence in 3' untranslated region

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<210> 244
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<212> DNA
<213> West Nile virus

<220>
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      conserved sequence in 3' untranslated region

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<210> 245
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<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF481864 region of
      conserved sequence in 3' untranslated region

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caccacaaca aaacagcata ttgacacctg ggatagacta ggaga             105

<210> 246
<211> 103
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain M12294 region of
      conserved sequence in 3' untranslated region

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acaaaagaa acagcatatt gacacctggg atagactagg gga                 103

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<210> 247  
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<220>  
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conserved sequence in 3' untranslated region

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<210> 249  
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<210> 251  
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<220>  
<223> West Nile virus strain AF404753 region of  
conserved sequence in 3' untranslated region

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<400> 251
tgctgaagc tgttagtcag gggaggact agaggttagt ggagaccccg tgccacaaaa 60
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 252
<211> 105
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404754 region of
      conserved sequence in 3' untranslated region

<400> 252
tgctgaagc tgttagtcag gggaggact agaggttagt ggagaccccg tgccacaaaa 60
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 253
<211> 105
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404755 region of
      conserved sequence in 3' untranslated region

<400> 253
tgctgaagc tgttagtcag gggaggact agaggttagt ggagaccccg tgccacaaaa 60
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 254
<211> 105
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF404756 region of
      conserved sequence in 3' untranslated region

<400> 254
tgctgaagc tgttagtcag gggaggact agaggttagt ggagaccccg tgccacaaaa 60
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 255
<211> 105
<212> DNA
<213> West Nile virus

<220>
<223> West Nile virus strain AF017254 region of
      conserved sequence in 3' untranslated region

<400> 255
tgactgaagc tgttagtcag gggaggact agaggttagt ggagaccccg tgccacaaaa 60
caccacaaca aaacagcata ttgataccctg ggatagacta ggaga 105

<210> 256
<211> 105
<212> DNA
<213> West Nile virus

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<220>  
<223> West Nile virus strain AF533540 region of  
conserved sequence in 3' untranslated region

<400> 256  
tgctgaagc tgttagtcag gggaggact agaggttagt ggagaccccg tgccacaaaa 60  
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 257  
<211> 105  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AY262283 region of  
conserved sequence in 3' untranslated region

<400> 257  
tgctgaagc tgttagtcag gggaggact agaggttagt ggagaccccg tgccgacaaaa 60  
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 258  
<211> 105  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AY278441 region of  
conserved sequence in 3' untranslated region

<400> 258  
tgctgaagc tgttagtcag gggaggact agaggttagt ggagaccccg tgccacaaaa 60  
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 259  
<211> 105  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AY268132 region of  
conserved sequence in 3' untranslated region

<400> 259  
tgctgaagc tgttagtcag gggaggact agaggttagt ggagaccccg tgccacaaaa 60  
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 260  
<211> 105  
<212> DNA  
<213> West Nile virus

<220>  
<223> West Nile virus strain AY268133 region of  
conserved sequence in 3' untranslated region

<400> 260  
tgctgaagc tgttagtcag gggaggact agaggttagt ggagaccccg tgccacaaaa 60  
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

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<210> 261
<211> 105
<212> DNA
<213> Kunjin virus

<220>
<223> Kunjin virus strain AY274504 region of conserved
      sequence in 3' untranslated region

<400> 261
tgctgaagc tggtagtcag gggaggact agaggttagt ggagaccccg tgccgcaaaa 60
caccacaaca acacagcata ttgacacctg ggatagacta ggaga           105

<210> 262
<211> 105
<212> DNA
<213> Kunjin virus

<220>
<223> Kunjin virus strain AY274505 region of conserved
      sequence in 3' untranslated region

<400> 262
tgctgaagc tggtagtcag gggaggact agaggttagt ggagaccccg tgccgcaaaa 60
caccacaaca acacagcata ttgacacctg ggatagacta ggaga           105

<210> 263
<211> 105
<212> DNA
<213> Kunjin virus

<220>
<223> Kunjin virus strain L24512 region of conserved
      sequence in 3' untranslated region

<400> 263
tgctgaagc tggtagtcag gggaggact agaggttagt ggagaccccg tgccgcaaaa 60
caccacaaca acacagcata ttgacacctg ggatagacta ggaga           105

<210> 264
<211> 99
<212> DNA
<213> Japanese encephalitis virus

<220>
<223> Japanese encephalitis virus strain AB051292 region
      of conserved sequence in 3' untranslated region

<400> 264
cccctcgaag ctgtggagga ggtggaaagga ctagaggtta gaggagaccc cgcatggca 60
tcaaaacagc atattgacac ctggaaatag actgggaga           99

<210> 265
<211> 98
<212> DNA
<213> Japanese encephalitis virus

<220>
<223> Japanese encephalitis virus strain AF014160 region
      of conserved sequence in 3' untranslated region

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<400> 265  
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tcaaacagca tattgacacc tggaataga ctgggaga 98

<210> 266  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF014161 region  
of conserved sequence in 3' untranslated region

<400> 266  
cccccgtcgaa ctgttagagga ggtggaagga ctagaggta gaggagaccc cgcatggca 60  
tcaaacagca tattgacacc tggaataga ctgggaga 98

<210> 267  
<211> 99  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF045551 region  
of conserved sequence in 3' untranslated region

<400> 267  
cccccgtcgaa ctgttagagga ggtgtaagga atagaggta gaggagaccc cgcaatttgca 60  
atcaaacagc atattgacac ctggaatag agtgggaga 99

<210> 268  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF069076 region  
of conserved sequence in 3' untranslated region

<400> 268  
cccccgtcgaa ctgttagagga ggtggaagga ctagaggta gaggagaccc cgcatggca 60  
tcaaacagca tattgacacc tggaataga ctgggaga 98

<210> 269  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF075723 region  
of conserved sequence in 3' untranslated region

<400> 269  
cccccgtcgaa ctgttagagga ggtggaagga ctagaggta gaggagaccc cgcatggca 60  
tcaaacagca tattgacacc tggaataga ctgggaga 98

<210> 270  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF080251 region  
of conserved sequence in 3' untranslated region

<400> 270  
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tcaaacagca tattgacacc tggaaataga ctgggaga 98

<210> 271  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF098735 region  
of conserved sequence in 3' untranslated region

<400> 271  
ctccctcgaa ctgttagagga ggtggaagga ctagaggta gaggagaccc cgcatggca 60  
tcaaacagca tattgacacc tggaaataga ctgggaga 98

<210> 272  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF098736 region  
of conserved sequence in 3' untranslated region

<400> 272  
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tcaaacagca tattgacacc tggaaataga ctgggaga 98

<210> 273  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF098737 region  
of conserved sequence in 3' untranslated region

<400> 273  
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tcaaacagca tattgacacc tggagataga ctgggaga 98

<210> 274  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF217620 region  
of conserved sequence in 3' untranslated region

<400> 274  
ttccctcgaa ctgttagagga agtggaaagga ctagaggta gaggagaccc cgcatggca 60  
tcaaacagca tattgacacc tggaaataga ctgggaga 98

<210> 275  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF221499 region  
of conserved sequence in 3' untranslated region

<400> 275  
ctcctcgaag ctgttagagga ggtggaagga ctagaggta gaggagaccc cgcatggca 60  
tcaaacagca tattgacacc tgaaataga ctgggaga 98

<210> 276  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF221500 region  
of conserved sequence in 3' untranslated region

<400> 276  
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tcaaacagca tattgacacc tgaaataga ctgggaga 98

<210> 277  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF254452 region  
of conserved sequence in 3' untranslated region

<400> 277  
cccctcgaag ctgttagagga ggtggaagga ctagaggta gaggagaccc cgcatggca 60  
tcaaacagca tattgacacc tgaaataga ctgggaga 98

<210> 278  
<211> 98  
<212> DNA  
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<220>  
<223> Japanese encephalitis virus strain AF254453 region  
of conserved sequence in 3' untranslated region

<400> 278  
cccctcgaag ctgttagagga ggtggaagga ctagaggta gaggagaccc cgcatggca 60  
tcaaacagca tattgacacc tgaaataga ctgggaga 98

<210> 279  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF315119 region  
of conserved sequence in 3' untranslated region

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<400> 279
cccctcgaag ctgttagagga ggtggaagga ctagaggtta gaggagaccc cgcatggca 60
tcaaacagca tattgacacc tggaataga ctgggaga 98

<210> 280
<211> 98
<212> DNA
<213> Japanese encephalitis virus

<220>
<223> Japanese encephalitis virus strain AF416457 region
      of conserved sequence in 3' untranslated region

<400> 280
cccctcgaag ctgttagagga ggtggaagga ctagaggtta gaggagaccc cgcatggca 60
tcaaacagca tattgacacc tggaataga ctgggaga 98

<210> 281
<211> 98
<212> DNA
<213> Japanese encephalitis virus

<220>
<223> Japanese encephalitis virus strain AF486638 region
      of conserved sequence in 3' untranslated region

<400> 281
cccctcgaag ctgttagagga ggtggaagga ctagaggtta gaggagaccc cgcatggca 60
tcaaacagca tattgacacc tggaatata ctgggaga 98

<210> 282
<211> 98
<212> DNA
<213> Japanese encephalitis virus

<220>
<223> Japanese encephalitis virus strain U14163 region
      of conserved sequence in 3' untranslated region

<400> 282
cccctcgaag ctgttagagga ggtggaagga ctagaggtta gaggagaccc cgcatggca 60
tcaaacagca tattgacacc tggaataga ctgggaga 98

<210> 283
<211> 98
<212> DNA
<213> Japanese encephalitis virus

<220>
<223> Japanese encephalitis virus strain U15763 region
      of conserved sequence in 3' untranslated region

<400> 283
cccctcgaag ctgttagagga ggtggaagga ctagaggtta gaggagaccc cgcatggca 60
tcaaacagca tattgacacc tggaataga ctgggaga 98

<210> 284
<211> 98
<212> DNA
<213> Japanese encephalitis virus

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<220>
<223> Japanese encephalitis virus strain L48961 region
      of conserved sequence in 3' untranslated region

<400> 284
ccctcgaag ctgttagagga ggtggaagga ctagaggtta gaggagaccc cgcatggca 60
tcaaacagca tattgacacc tggaaataga ctgggaga                         98

<210> 285
<211> 98
<212> DNA
<213> Japanese encephalitis virus

<220>
<223> Japanese encephalitis virus strain U47032 region
      of conserved sequence in 3' untranslated region

<400> 285
ccctcgaag ctgttagagga ggtggagggta ctagaggtta gaggagaccc cgcatggca 60
tcaaacagca tattgacacc tggaaataga ctgggaga                         98

<210> 286
<211> 98
<212> DNA
<213> Japanese encephalitis virus

<220>
<223> Japanese encephalitis virus strain M18370 region
      of conserved sequence in 3' untranslated region

<400> 286
ccctcgaag ctgttagagga ggtggaagga ctagaggtta gaggagaccc cgcatggca 60
tcaaacagca tattgacacc tggaaataga ctgggaga                         98

<210> 287
<211> 98
<212> DNA
<213> Japanese encephalitis virus

<220>
<223> Japanese encephalitis virus strain M55506 region
      of conserved sequence in 3' untranslated region

<400> 287
ccctcgaag ctgttagagga ggtggaagga ctagaggtta gaggagaccc cgcatggca 60
tcaaacagca tattgacacc tggaaataga ctgggaga                         98

<210> 288
<211> 98
<212> DNA
<213> Japanese encephalitis virus

<220>
<223> Japanese encephalitis virus strain L78128 region
      of conserved sequence in 3' untranslated region

<400> 288
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tcaaacagca tattgacacc tggaaataga ctgggaga                         98

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<210> 289  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain D90195 region  
of conserved sequence in 3' untranslated region

<400> 289  
cccctcgaag ctgttagagga ggtggaagga ctagaggtta gaggagaccc cgcatggca 60  
tcaaacagca tattgacacc tgaaataga ctgggaga 98

<210> 290  
<211> 98  
<212> DNA  
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<220>  
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of conserved sequence in 3' untranslated region

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tcaaacagca tattgacacc tgaaataga ctgggaga 98

<210> 291  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF311748 region  
of conserved sequence in 3' untranslated region

<400> 291  
cccctcgaag ctgttagagga ggtggaagga ctagaggtta gaggagaccc cgcatggca 60  
tcaaacagca tattgacacc tgaaataga ctgggaga 98

<210> 292  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AY184212 region  
of conserved sequence in 3' untranslated region

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tcaaacagca tattgacacc tgaaataga ctgggaga 98

<210> 293  
<211> 99  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AY316157 region  
of conserved sequence in 3' untranslated region

<400> 293  
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atcaaacagc atattgacac ctggaatag actgggaga 99

<210> 294  
<211> 99  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF306514 region  
of conserved sequence in 3' untranslated region

<400> 294  
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atcaaacagc atattgacac ctggaatag agtgggaga 99

<210> 295  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF306515 region  
of conserved sequence in 3' untranslated region

<400> 295  
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tcaaacagca tattgacacc tgaaataga ctgggaga 98

<210> 296  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF306516 region  
of conserved sequence in 3' untranslated region

<400> 296  
ccctcgaag ctgttagaggg ggtggaagga ctagaggta gaggagaccc cgcatttgca 60  
tcaaacagca tattgacacc tgaaataga ctgggaga 98

<210> 297  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
<223> Japanese encephalitis virus strain AF306517 region  
of conserved sequence in 3' untranslated region

<400> 297  
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tcaaacagca tattgacacc tgaaataga gtgggaga 98

<210> 298  
<211> 98  
<212> DNA  
<213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain D00037 region  
     of conserved sequence in 3' untranslated region

<400> 298  
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 tcaaacagca tattgacacc tggaataga ctgggaga 98

<210> 299  
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 <212> DNA  
 <213> Japanese encephalitis virus

<220>  
 <223> Japanese encephalitis virus strain M14933 region  
     of conserved sequence in 3' untranslated region

<400> 299  
 cctctttagt ctttgaggt ggttgaaggt cttgagggtt gaggagtccc cgtctttgca 60  
 tcaaacagca tattgacacc tggaataga ctgggaga 98

<210> 300  
 <211> 100  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain BFS1750-C  
     region of conserved sequence in 3' untranslated  
     region

<400> 300  
 ccgcgtcgaa ctgttagagac gggggaaagga ctagagggtt gaggagaccc cttgccgtta 60  
 acgcaaacaa cagcatattg acacctggaa agacaggaga 100

<210> 301  
 <211> 27  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain 1750-Std  
     region of conserved sequence in 3' untranslated  
     region

<400> 301  
 ccgcgtcgaa ctgttagagac gggggaa 27

<210> 302  
 <211> 100  
 <212> DNA  
 <213> St. Louis encephalitis virus

<220>  
 <223> St. Louis encephalitis virus strain TD6-4G-C  
     region of conserved sequence in 3' untranslated  
     region

<400> 302  
 ccgcgtcgaa ctgttagagat gggggaaagga ctagagggtt gaggagaccc cttgccgtta 60  
 acgcaaacaa cagcatattg acacctggaa agacaggaga 100

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<210> 303
<211> 100
<212> DNA
<213> St. Louis encephalitis virus

<220>
<223> St. Louis encephalitis virus strain TD6-4G-20
      region of conserved sequence in 3' untranslated
      region

<400> 303
ccgctcgaag ctgttagat ggggaaagga ctagaggta gaggagaccc cttgccgtta 60
acgcaaaca cagcatattg acacctggaa agacaggaga 100

<210> 304
<211> 27
<212> DNA
<213> St. Louis encephalitis virus

<220>
<223> St. Louis encephalitis virus strain CoaV750
      region of conserved sequence in 3' untranslated
      region

<400> 304
ccgctcgaag ctgttagat ggggaa 27

<210> 305
<211> 100
<212> DNA
<213> St. Louis encephalitis virus

<220>
<223> St. Louis encephalitis virus strain L695121.05
      region of conserved sequence in 3' untranslated
      region

<400> 305
ccgctcgaag ctgttagac ggggaaagga ctagaggta gaggagaccc cttgccgtta 60
acgcaaaca cagcatattg acacctggaa agacaggaga 100

<210> 306
<211> 100
<212> DNA
<213> St. Louis encephalitis virus

<220>
<223> St. Louis encephalitis virus strain TNM771K-C
      region of conserved sequence in 3' untranslated
      region

<220>
<221> modified base
<222> (68) ... (68)
<223> n = g, a, c or t

<400> 306
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acgcaaanaa cagcatattg acacctggaa agacaggaga 100

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<210> 307  
<211> 100  
<212> DNA  
<213> St. Louis encephalitis virus

<220>  
<223> St. Louis encephalitis virus strain MSI-7-C  
region of conserved sequence in 3' untranslated  
region

<400> 307  
ccgctcaaag ctgttagagac ggggaaagga ctagaggta gaggagaccc cttgccgtta 60  
acgcaaacaa cagcatattg acacctggaa agacaggaga 100

<210> 308  
<211> 95  
<212> DNA  
<213> St. Louis encephalitis virus

<220>  
<223> St. Louis encephalitis virus strain Kern217  
region of conserved sequence in 3' untranslated  
region

<400> 308  
ccgctcaaag ctgttagagac ggggaaagga ctagaggta gaggagaccc cttgccgtta 60  
acgcaaacaa cagcatattg acacctggaa agaca 95

<210> 309  
<211> 100  
<212> DNA  
<213> St. Louis encephalitis virus

<220>  
<223> St. Louis encephalitis virus strain CoaV608  
region of conserved sequence in 3' untranslated  
region

<400> 309  
ccgctcaaag ctgttagagac ggggaaagga ctagaggta gaggagaccc cttgccgtta 60  
acgcaaacaa cagcatattg acacctggaa agacaggaga 100

<210> 310  
<211> 95  
<212> DNA  
<213> St. Louis encephalitis virus

<220>  
<223> St. Louis encephalitis virus strain TBH-28  
region of conserved sequence in 3' untranslated  
region

<400> 310  
ccgctcgaag ctgttagagac ggggaaagga ctagaggta gaggagaccc cttgccgtta 60  
acgcaaacaa cagcatattg acacctggaa agaca 95

<210> 311  
<211> 92  
<212> DNA  
<213> St. Louis encephalitis virus

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<220>
<223> St. Louis encephalitis virus strain VR1265
      region of conserved sequence in 3' untranslated
      region

<400> 311
ccgctcgaag ctgttagagac ggggaaagga ctagaggta gaggagaccc cttgccgtca 60
acgcaaacaa cagcatattg acacctggaa ag                                92

<210> 312
<211> 100
<212> DNA
<213> St. Louis encephalitis virus

<220>
<223> St. Louis encephalitis virus strain CoaV353
      region of conserved sequence in 3' untranslated
      region

<400> 312
ccgctcgaag ctgttagagac ggggaaagga ctagaggta gaggagaccc cttgccgtta 60
acgcaaacaa cagcatattg acacctggaa agacaggaga                                100

<210> 313
<211> 104
<212> DNA
<213> Murray Valley encephalitis virus

<220>
<223> Murray Valley encephalitis virus strain VR77
      region of conserved sequence in 3' untranslated
      region

<400> 313
tcgcgaagc tgtaaggcgg gtggacggac tagaggtag aggagacccc actctaaaa 60
gcatcaaaca acagcatatt gacacctggg aaaagactag gaga                                104

<210> 314
<211> 104
<212> DNA
<213> Murray Valley encephalitis virus

<220>
<223> Murray Valley encephalitis virus strain AF161266
      region of conserved sequence in 3' untranslated
      region

<400> 314
tcgcgaagc tgtaaggcgg gtggacggac tagaggtag aggagacccc actctaaaa 60
gcatcaaaca acagcatatt gacacctggg aaaagactag gaga                                104

<210> 315
<211> 100
<212> DNA
<213> Murray Valley encephalitis virus

<220>
<223> Murray Valley encephalitis virus strain M35172
      region of conserved sequence in 3' untranslated
      region

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<400> 315  
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<210> 316  
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<212> DNA  
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<220>  
<223> West Nile virus strain AF260967 region of  
conserved sequence in 3' untranslated region

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a 121

<210> 317  
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<212> DNA  
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<220>  
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a 121

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a 121

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<212> DNA  
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a 121

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a 121

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<212> DNA  
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a 121

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a 121

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<220>  
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conserved sequence in 3' untranslated region

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a 121

<210> 330
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ggctgaagct gtaagccaag ggaagga 87

<210> 331
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a 121

<210> 332
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<220>
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a 121

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<210> 337  
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a 121

<210> 338
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a 121

<210> 339
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<212> DNA
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<220>
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a 121

<210> 341
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<220>
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a 121

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a 121

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catca 125

<210> 347  
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of conserved sequence in 3' untranslated region

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atcaa 125

<210> 349  
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of conserved sequence in 3' untranslated region

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atcaa 125

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atcaa 125

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of conserved sequence in 3' untranslated region

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atcaa 125

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of conserved sequence in 3' untranslated region

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of conserved sequence in 3' untranslated region

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atcaa 125

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of conserved sequence in 3' untranslated region

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<220>

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catca 125

<210> 373  
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<220>

<223> Japanese encephalitis virus strain AF306514 region  
of conserved sequence in 3' untranslated region

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<210> 374  
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<212> DNA  
<213> Japanese encephalitis virus

<220>

<223> Japanese encephalitis virus strain AF306515 region  
of conserved sequence in 3' untranslated region

<400> 374  
cgaggtgtaa ggactagagg ttagaggaga ccccgtaaa acaaaaaaat gcgccccaaag 60  
ccccctcgaa gctgttagagg aggtgaaagg actagaggtt agaggagacc ccgcatttg 120  
atcaa 125

<210> 375  
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<212> DNA  
<213> Japanese encephalitis virus

<220>

<223> Japanese encephalitis virus strain AF306516 region  
of conserved sequence in 3' untranslated region

<400> 375  
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atcaa 125

<210> 376  
<211> 125  
<212> DNA  
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<220>

<223> Japanese encephalitis virus strain AF306517 region  
of conserved sequence in 3' untranslated region

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<400> 376
cgaggtgtaa ggactagagg ttagaggaga ccccgctggaa acaaaaaat gcggcccaag 60
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atcaa                                              125

<210> 377
<211> 122
<212> DNA
<213> St. Louis encephalitis virus

<220>
<223> St. Louis encephalitis virus strain BFS1750 region
      of conserved sequence in 3' untranslated region

<400> 377
catggcgtaa ggactagagg ttagaggaga ccccgctgca acttggcaag gcccaaaccc 60
gctcgaagct gtagagacgg gggaaaggact agaggttaga ggagacccct tgccgttaac 120
gc                                              122

<210> 378
<211> 85
<212> DNA
<213> St. Louis encephalitis virus

<220>
<223> St. Louis encephalitis virus strain 1750-Std region
      of conserved sequence in 3' untranslated region

<400> 378
catggcgtaa ggactagagg ttagaggaga ccccgckgca acttggcaag gcccaaaccc 60
gctcgaagct gtagagacgg gggaa                                              85

<210> 379
<211> 122
<212> DNA
<213> St. Louis encephalitis virus

<220>
<223> St. Louis encephalitis virus strain TD6-4G region
      of conserved sequence in 3' untranslated region

<400> 379
catggcgtaa ggactagagg ttagaggaga ccccgctgca actcggcaag gcccaaaccc 60
gctcgaagct gtagagatgg gggaaaggact agaggttaga ggagacccct tgccgttaac 120
gc                                              122

<210> 380
<211> 85
<212> DNA
<213> St. Louis encephalitis virus

<220>
<223> St. Louis encephalitis virus strain CoaV750 region
      of conserved sequence in 3' untranslated region

<400> 380
catggcgtaa ggactagagg ttagaggaga ccccgckgca acttggcaag gccaaaaccc 60
gctcgaagct gtagagatgg gggaa                                              85

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<210> 381  
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<220>  
<223> St. Louis encephalitis virus strain L695121.05 region  
of conserved sequence in 3' untranslated region

<400> 381  
catggcgtaa ggactagagg ttagaggaga ccccgctgta acttggcaag gcccaaacc 60  
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gc 122

<210> 382  
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<212> DNA  
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<220>  
<223> St. Louis encephalitis virus strain TNM771K region  
of conserved sequence in 3' untranslated region

<400> 382  
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gc 122

<210> 383  
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<220>  
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of conserved sequence in 3' untranslated region

<400> 383  
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gc 122

<210> 384  
<211> 122  
<212> DNA  
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<220>  
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of conserved sequence in 3' untranslated region

<400> 384  
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gc 122

<210> 385  
<211> 122  
<212> DNA  
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<220>  
<223> St. Louis encephalitis virus strain CoaV608 region  
of conserved sequence in 3' untranslated region

<400> 385  
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gc 122

<210> 386  
<211> 122  
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<220>  
<223> St. Louis encephalitis virus strain TBH-28 region  
of conserved sequence in 3' untranslated region

<400> 386  
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gc 122

<210> 387  
<211> 122  
<212> DNA  
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<220>  
<223> St. Louis encephalitis virus strain VR1265 region  
of conserved sequence in 3' untranslated region

<400> 387  
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gc 122

<210> 388  
<211> 122  
<212> DNA  
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<220>  
<223> St. Louis encephalitis virus strain CoaV353 region  
of conserved sequence in 3' untranslated region

<400> 388  
catggcgtaa ggactagagg ttagaggaga ccccgctgca acttggcaag gcccaaacc 60  
gctcgaagct gtagagacgg gggaggact agaggttaga ggagacccct tgccgttaac 120  
gc 122

<210> 389  
<211> 119  
<212> DNA  
<213> Murray Valley encephalitis virus

<220>  
<223> Murray Valley encephalitis virus strain VR77  
region of conserved sequence in 3' untranslated  
region

<400> 389  
 cccggcgaag gactagaggt tagaggagac cctgcggaag aaatgagtgg cccaagctcg 60  
 cccaagctgt aaggcgggtg gacggactag agtttagagg agaccccaact ctcaaaagc 119

<210> 390  
 <211> 119  
 <212> DNA  
 <213> Murray Valley encephalitis virus

<220>  
 <223> Murray Valley encephalitis virus strain AF161266  
 region of conserved sequence in 3' untranslated  
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<400> 390  
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 cccaagctgt aaggcgggtg gacggactag agtttagagg agaccccaact ctcaaaagc 119

<210> 391  
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<220>  
 <223> Murray Valley encephalitis virus strain M35172  
 region of conserved sequence in 3' untranslated  
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<400> 391  
 cccggcgaag gactagaggt tagaggagac cctgcggaag aaatgagtgg cccaagctcg 60  
 cccaagctgt aaggcgggtg gacggactag agtttagagg agaccccaact ctcaaaagc 119

<210> 392  
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<220>  
 <223> Dengue virus type 1 strain U88537 region of  
 conserved sequence in 3' untranslated region

<400> 392  
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 cccaacacca gggaaagctg taccctggtg gtaaggacta gaggttagag gagacccccc 120  
 gcacaacaac a 131

<210> 393  
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<220>  
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 gcacaacaac a 131

<210> 394  
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<220>  
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conserved sequence in 3' untranslated region

<400> 394  
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gcacaacaac a 131

<210> 395  
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<220>  
<223> Dengue virus type 1 strain M87512 region of  
conserved sequence in 3' untranslated region

<400> 395  
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gcataacaat a 131

<210> 396  
<211> 131  
<212> DNA  
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<220>  
<223> Dengue virus type 1 strain AY206457 region of  
conserved sequence in 3' untranslated region

<400> 396  
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cccaacacca gggaaagctg tacctggtg gtaaggacta gaggttagag gagacccccc 120  
gcacaacaac a 131

<210> 397  
<211> 101  
<212> DNA  
<213> Dengue virus type 1

<220>  
<223> Dengue virus type 1 strain AY145123 region of  
conserved sequence in 3' untranslated region

<400> 397  
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cccaagacta gaggttagag gagacccccc gcacaacaac a 101

<210> 398  
<211> 131  
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<220>  
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conserved sequence in 3' untranslated region

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gcacaacaac a 131

<210> 399  
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<220>  
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conserved sequence in 3' untranslated region

<400> 399  
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gcacaacaac a 131

<210> 400  
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<220>  
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conserved sequence in 3' untranslated region

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gcacaacaac a 131

<210> 401  
<211> 131  
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<213> Dengue virus type 1

<220>  
<223> Dengue virus type 1 strain AF514885 region of  
conserved sequence in 3' untranslated region

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gcataacaac a 131

<210> 402  
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<213> Dengue virus type 1

<220>  
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conserved sequence in 3' untranslated region

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gcataacaac a 131

<210> 403
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
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gcacaacaac a 131

<210> 404
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
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      conserved sequence in 3' untranslated region

<400> 404
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gcataacaac a 131

<210> 405
<211> 131
<212> DNA
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<220>
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gcacaacaac a 131

<210> 406
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
<223> Dengue virus type 1 strain AF350498 region of
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<400> 406
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gcataacaat a 131

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<210> 407
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
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<400> 407
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cccaacacca tggaaagctg taccttggtg gtaaggacta gaggttagag gagacccccc 120
gctcaacaac a 131

<210> 408
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
<223> Dengue virus type 1 strain AF311957 region of
      conserved sequence in 3' untranslated region

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cccaacacca tggaaagctg taccttggtg gtaaggacta gaggttagag gagacccccc 120
gcacaacaac a 131

<210> 409
<211> 131
<212> DNA
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<220>
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gcacaacaac a 131

<210> 410
<211> 97
<212> DNA
<213> Dengue virus type 1

<220>
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cccaacacca gggaaagctg taccctggtg gtaagga 97

<210> 411
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<212> DNA
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<220>
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cccaacacca gggaaagctg taccctggtg gtaaggacta gaggttagag gagacccccc 120
gcataacaat a                                         131

<210> 412
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
<223> Dengue virus type 1 strain AF310146 region of
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cccaacacca tggaaagctg taccttggtg gtaaggacta gaggttagag gagacccccc 120
gcacaacaac a                                         131

<210> 413
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
<223> Dengue virus type 1 strain AF309641 region of
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cccaacacca gggaaagctg taccctggtg gtaaggacta gaggttagag gagacccccc 120
gcataacaat a                                         131

<210> 414
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
<223> Dengue virus type 1 strain AF298808 region of
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gcataacaat a                                         131

<210> 415
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gcacaacaac a 131

<210> 416
<211> 131
<212> DNA
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gcacaacaac a 131

<210> 417
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
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cccaacacca ggggaagctg taccttggtg gtaaggacta gaggttagag gagacccccc 120
gcacaacaac a 131

<210> 418
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
<223> Dengue virus type 1 strain AF226685 region of
      conserved sequence in 3' untranslated region

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cccaacacca tgggaagctg taccttggtg gtaaggacta gaggttagag gagacccccc 120
gcacaacaac a 131

<210> 419
<211> 131
<212> DNA
<213> Dengue virus type 1

<220>
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      conserved sequence in 3' untranslated region

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cccaacacca ggggaagctg taccctggtg gtaaggacta gaggttagag gagacccccc 120
gcgtaaacaat a 131

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<210> 420  
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<220>  
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conserved sequence in 3' untranslated region

<400> 420  
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gcataacaat a 131

<210> 421  
<211> 131  
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<220>  
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conserved sequence in 3' untranslated region

<400> 421  
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gcataataat a 131

<210> 422  
<211> 131  
<212> DNA  
<213> Dengue virus type 1

<220>  
<223> Dengue virus type 1 strain AB074760 region of  
conserved sequence in 3' untranslated region

<400> 422  
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gcataacaat a 131

<210> 423  
<211> 131  
<212> DNA  
<213> Dengue virus type 1

<220>  
<223> Dengue virus type 1 strain VR344-3 region of  
conserved sequence in 3' untranslated region

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cccaacacca gggaaagctg taccctggtg gtaaggacta gaggttagag gagacccccc 120  
gcataacaat a 131

<210> 424  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF022434 region of  
conserved sequence in 3' untranslated region

<400> 424  
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ggcccaagg cgagatgaag ctgttgtctc gctggaagga ctagaggtta gaggagaccc 120  
ccccgaaaca gaa 133

<210> 425  
<211> 133  
<212> DNA  
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<220>  
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conserved sequence in 3' untranslated region

<400> 425  
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ccccgaaaca aaa 133

<210> 426  
<211> 133  
<212> DNA  
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<220>  
<223> Dengue virus type 2 strain AF022436 region of  
conserved sequence in 3' untranslated region

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ggcccaagg cgagatgaag ctgttgtctc gctggaagga ctagaggtta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 427  
<211> 133  
<212> DNA  
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<220>  
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conserved sequence in 3' untranslated region

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ggcccaagg cgagatgaag ctgttgtctc gctggaagga ctagaggtta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 428  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF022438 region of  
conserved sequence in 3' untranslated region

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<400> 428
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ggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
ccccgaaaca aaa 133

<210> 429
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF022439 region of
      conserved sequence in 3' untranslated region

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ggcccaagg cgagatgaag ctgtagtctc gctggaagga atagaggtta gaggagaccc 120
ccccgaaaca aaa 133

<210> 430
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF022440 region of
      conserved sequence in 3' untranslated region

<400> 430
atggcgtagt ggactagcggttagaggaga cccctccctc acaaatcgca gcaacaatgg 60
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ccccgaaaca aaa 133

<210> 431
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF022441 region of
      conserved sequence in 3' untranslated region

<400> 431
atggcgtagt ggactagcggttagaggaga cccctccctc acaaatcgca gcaacaatgg 60
ggcccaagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120
ccccgaaaca aaa 133

<210> 432
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF038402 region of
      conserved sequence in 3' untranslated region

<400> 432
atggcgtagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60
ggcccaagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120
ccccaaaaca aaa 133

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<210> 433  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF038403 region of  
conserved sequence in 3' untranslated region

<400> 433  
atggcgtagt ggactagcg ttagaggaga cccctccctt acaaatcgca gcaacaatgg 60  
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120  
ccccaaaaca aaa 133

<210> 434  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF100145 region of  
conserved sequence in 3' untranslated region

<400> 434  
atggcgtagt ggactagcg ttagaggaga cccctccctt acaaatcgca gcaacaacgg 60  
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120  
ccccaaaata aaa 133

<210> 435  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF100146 region of  
conserved sequence in 3' untranslated region

<400> 435  
atggcgtagt ggactagcg ttagaggaga cccctccctt acaaatcgca gcaacaatgg 60  
ggcccaagg cgagatgaag ctgtgtctc gctggaagga ctagaggtta gaggagaccc 120  
ccccgaagca aaa 133

<210> 436  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF100147 region of  
conserved sequence in 3' untranslated region

<400> 436  
atggcgtagt ggactagcg ttagaggaga cccctccctt acaaatcgca gcaacaatgg 60  
ggcccaagg cgagatgaag ctgtgtctc gctggaagga ctagaggtta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 437  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF100148 region of  
conserved sequence in 3' untranslated region

<400> 437  
atggtagtggactagcggttagaggaga cccctcccttcagatcgca gcaacaatgg 60  
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120  
ccccaaaaca aaa 133

<210> 438  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF100149 region of  
conserved sequence in 3' untranslated region

<400> 438  
atggcgttagt ggactagcggttagaggaga cccctccctt acagatcgca gcaacaatgg 60  
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ccccaaaaca aaa 133

<210> 439  
<211> 133  
<212> DNA  
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<220>  
<223> Dengue virus type 2 strain AF100150 region of  
conserved sequence in 3' untranslated region

<400> 439  
atggcgttagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaacgg 60  
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120  
ccccaaaaca aaa 133

<210> 440  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF100151 region of  
conserved sequence in 3' untranslated region

<400> 440  
atggcgttagt ggactagcggttagaggaga cccctccctt acagatcgca gcaacaatgg 60  
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120  
ccccaaagaca aaa 133

<210> 441  
<211> 134  
<212> DNA  
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<220>  
<223> Dengue virus type 2 strain AF100458 region of  
conserved sequence in 3' untranslated region

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<400> 441
atggcgtagt ggactagcggttagaggaga cccctccctt acagatcgca gcaacaatgg 60
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggta gaggagaccc 120
ccccaaaaac aaaa 134

<210> 442
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF100459 region of
      conserved sequence in 3' untranslated region

<400> 442
atggcgtagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60
ggcccaagg cgagatgaag ctgtgtctc gctggaagga ctagaggta gaggagaccc 120
ccccgaaaca aaa 133

<210> 443
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF100460 region of
      conserved sequence in 3' untranslated region

<400> 443
atggcgtagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60
ggcccaagg cgagatgaag ctgtgtctc gctggaagga ctagaggta gaggagaccc 120
ccccgaaaca aaa 133

<210> 444
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF100461 region of
      conserved sequence in 3' untranslated region

<400> 444
atggcgtagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60
ggcccaagg cgagatgaag ctgtgtctc gctggaagga ctagaggta gaggagaccc 120
ccccgaaaca aaa 133

<210> 445
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF100462 region of
      conserved sequence in 3' untranslated region

<400> 445
atggcgtagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60
ggcccaagg cgagatgaag ctgtgtctc gctggaagga ctagaggta gaggagaccc 120
ccccgaaaca aaa 133

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<210> 446
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF100463 region of
      conserved sequence in 3' untranslated region

<400> 446
atggcgtagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60
ggcccaagg cgagatgaag ctgtgtctc gctggaagga ctagaggtta gaggagaccc 120
ccccgaaaca aaa 133

<210> 447
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF100464 region of
      conserved sequence in 3' untranslated region

<400> 447
atggcgtagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60
ggcccaagg caagatgaag ctgtgtctc gctggaagga ctagaggtta gaggagaccc 120
ccccgaaaca aaa 133

<210> 448
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF100465 region of
      conserved sequence in 3' untranslated region

<400> 448
atggcgtagt ggactagcggttagaggaga cccctccctt acagatcgca gcaacaatgg 60
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120
ccccaaagaca aaa 133

<210> 449
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF100466 region of
      conserved sequence in 3' untranslated region

<400> 449
atggcgtagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaacgg 60
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120
ccccaaaata aaa 133

<210> 450
<211> 134
<212> DNA
<213> Dengue virus type 2

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<220>  
<223> Dengue virus type 2 strain AF100467 region of  
conserved sequence in 3' untranslated region

<400> 450  
atggcgtagt ggactagcggttagaggaga cccctccctt acagatcgca gcaacaatgg 60  
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120  
ccccaaaaaaa caaa 134

<210> 451  
<211> 134  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF100468 region of  
conserved sequence in 3' untranslated region

<400> 451  
atggcgtagt ggactagcggttagaggaga cccctccctt acagatcgca gcaacaatgg 60  
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120  
ccccaaaaaaa caaa 134

<210> 452  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF100469 region of  
conserved sequence in 3' untranslated region

<400> 452  
atggcgtagt ggactagcggttagaggaga cccctccctt tcagatcgca gcaacaatgg 60  
ggcccatgg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120  
ccccaaaaca aaa 133

<210> 453  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF119661 region of  
conserved sequence in 3' untranslated region

<400> 453  
atggcgtagg ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaacgg 60  
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gattagaccc 120  
ccccaaaaca aaa 133

<210> 454  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169687 region of  
conserved sequence in 3' untranslated region

<400> 454  
atggcgtagt ggactagcg tttagaggaga cccctccctc acaaatcgca gcaacaatgg 60  
ggcccaagg cgagatgaag ctgtgtctc gctggaagga ctagaggtta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 455  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169678 region of  
conserved sequence in 3' untranslated region

<400> 455  
atggcgtagt ggactagcg tttagaggaga cccctccctc acaaatcgca gcaacaatgg 60  
ggcccaagg cgagatgaag ctgtgtctc gctggaagga ctagaggtta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 456  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169688 region of  
conserved sequence in 3' untranslated region

<400> 456  
atggcgtagt ggactagcg tttagaggaga cccctccctc acaaatcgca gcaacaatgg 60  
ggcccaagg cgagatgaag ctgtgtctc gctggaagga ctagaggtta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 457  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169679 region of  
conserved sequence in 3' untranslated region

<400> 457  
atggcgtagt ggactagcg tttagaggaga cccctccctt acaaatcgca gcaacaatgg 60  
ggcccaaaag tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 458  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169680 region of  
conserved sequence in 3' untranslated region

<400> 458  
atggcgtagt ggactagcg tttagaggaga cccctccctc acaaatcgca gcaacaatgg 60  
ggcccaagg cgagatgaag ctgtgtctc gcttgaagga ctagaggtta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 459  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169681 region of  
conserved sequence in 3' untranslated region

<400> 459  
atggcgtagt ggactagcgg ttagaggaga cccctccctc acaaatcgca gcaacaatgg 60  
gggcccagg cgagatgaag ctgttagtctc gctggaagga ctagaggta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 460  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169682 region of  
conserved sequence in 3' untranslated region

<400> 460  
atggcgtagt ggactagcgg ttagaggaga cccctccctc acaaatcgca gcaacaatgg 60  
gggcccagg cgagatgaag ctgttagtctc gctggaagga ctagaggta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 461  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169683 region of  
conserved sequence in 3' untranslated region

<400> 461  
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gggcccagg cgagatgaag ctgttagtctc gctggaagga ctagaggta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 462  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169684 region of  
conserved sequence in 3' untranslated region

<400> 462  
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gggcccagg cgagatgaag ctgttagtctc gctggaagga ctagaggta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 463  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169685 region of  
conserved sequence in 3' untranslated region

<400> 463  
atggcgttagt ggactagcggttagaggaga cccctccctc acaaatcgca gcaacaatgg 60  
gggcccagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 464  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF169686 region of  
conserved sequence in 3' untranslated region

<400> 464  
atggcgttagt ggactagcggttagaggaga cccctccctc acaaatcgca gcaacaatgg 60  
gggcccagg cgagatgaag ctgtagtctc gctggaagga ctagaggtta gaggagaccc 120  
ccccgaaaca aaa 133

<210> 465  
<211> 133  
<212> DNA  
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<220>  
<223> Dengue virus type 2 strain AF204177 region of  
conserved sequence in 3' untranslated region

<400> 465  
atggcgttagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60  
gggcccagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120  
ccccaaaaca aaa 133

<210> 466  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF204178 region of  
conserved sequence in 3' untranslated region

<400> 466  
atggcgttagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60  
gggcccagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120  
ccccaaaaca aaa 133

<210> 467  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF208496 region of  
conserved sequence in 3' untranslated region

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<400> 467
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ccccaaaaca aaa 133

<210> 468
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF276619 region of
      conserved sequence in 3' untranslated region

<400> 468
atggcgtagt ggactagcggttagaggaga cccctccctt gcaaatcgca gcaacaatgg 60
ggcccaagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120
ccccgaaata aaa 133

<210> 469
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF309950 region of
      conserved sequence in 3' untranslated region

<400> 469
atggcgtagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60
ggcccaagg tgagatgaag ctgtagtctc actggaagga ctagaggtta gaggagaccc 120
ccccgaaata aaa 133

<210> 470
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF309951 region of
      conserved sequence in 3' untranslated region

<400> 470
atggcgtagt ggactagcggttagaggaga cccctccctt acagatcgca gcaacaacgg 60
ggcccaagg tgagataaag ctgtagtctc accggaagga ctagaggtta gaggagaccc 120
ccccaaaaca aaa 133

<210> 471
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF305592 region of
      conserved sequence in 3' untranslated region

<400> 471
atggcgtagt ggactagcggttagaggaga cccctccctt aagaatcgca gaaaaatggg 60
ggcccaaggt gtgttgaagc ttagccaca ctggaaggac cagaggttag aggagacccc 120
cccagacaaa aaa 133

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<210> 472
<211> 134
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF309953 region of
      conserved sequence in 3' untranslated region

<400> 472
gtggtagt ggactagcg tttagaggaga cccctccctt aagaatcgca gcaaaaatgg 60
ggcccaagg tgttgtgaag ctgtagccac actggaagga ctagaggtta gaggagaccc 120
ccccagacaa aaaa                                134

<210> 473
<211> 134
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF309954 region of
      conserved sequence in 3' untranslated region

<400> 473
atggtagt ggactagcg tttagaggaga cccctccctt aagaatcgca gcaaaaatgg 60
ggcccaagg tgttgtgaag ctgtagccac actggaagga ctagaggtta gaggagaccc 120
ccccagacaa aaaa                                134

<210> 474
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF309955 region of
      conserved sequence in 3' untranslated region

<400> 474
atggtagt ggactagcg tttagaggaga cccctccctt aagaatcgca gcaaaaattgg 60
ggcccaaggt gtgttgtaagc tgttagccaca ctggaggac cagaggttag aggagacccc 120
ccccagacaaa aaa                                133

<210> 475
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF309956 region of
      conserved sequence in 3' untranslated region

<400> 475
atggtagt ggactagcg tttagaggaga cccctccctt aagaatcgca gcaaaaatggg 60
ggcccaaggt gtgttgtaagc tgttagccaca ctggaggac cagaggttag aggagacccc 120
ccccagacaaa aaa                                133

<210> 476
<211> 133
<212> DNA
<213> Dengue virus type 2

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<220>  
<223> Dengue virus type 2 strain AF309957 region of  
conserved sequence in 3' untranslated region

<400> 476  
atgggtgtagt ggactagcggttagaggaga cccctccctt aagaatcgca gcaaaaatggg 60  
ggcccaagggt gtgttgaagc tgttagccaca ctggaaggac cagaggttag aggagacccc 120  
cccaagacaaa aaa 133

<210> 477  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF309958 region of  
conserved sequence in 3' untranslated region

<400> 477  
atggcgttgt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60  
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagacccc 120  
ccccgaaata aaa 133

<210> 478  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF309959 region of  
conserved sequence in 3' untranslated region

<400> 478  
atgggtgtagt ggactagcggttagaggaga cccctccctt aaaaatcgca gcaaaaaatgg 60  
ggcccaagg tgggttgaag ctgttagccac attggaagga ctagaggtta gaggagacccc 120  
ccccagacaaa aaa 133

<210> 479  
<211> 133  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF309960 region of  
conserved sequence in 3' untranslated region

<400> 479  
atggcgttgt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60  
ggcccaagg tgagatgaag ctgtgtctc actggaagga ctagaggtta gaggagacccc 120  
ccccgaaata aaa 133

<210> 480  
<211> 132  
<212> DNA  
<213> Dengue virus type 2

<220>  
<223> Dengue virus type 2 strain AF309961 region of  
conserved sequence in 3' untranslated region

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<400> 480
atggtagt ggactagcggttagaggaga cccctccctt aaggatcgca gcaaaatggg 60
ggcccaagggt gtggtaagc tgttagccaca ctggaaggac tagaggttag aggagacccc 120
ccccacaata at 132

<210> 481
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF309962 region of
      conserved sequence in 3' untranslated region

<400> 481
atggcgtagt ggactagcggttagaggaga cccctccctt gcaaatcgca gcaacaatgg 60
ggcccaagg tgagatgaag ctgttgtctc actggaagga ctagaggtta gaggagacccc 120
ccccgaaata aaa 133

<210> 482
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF309963 region of
      conserved sequence in 3' untranslated region

<400> 482
atggcgtagt ggactagcggttagaggaga cccctccctt acaagtcgca gcagcaatgg 60
ggcccaagg tgagatgaag ctgttgtctc actggaagga ctagaggtta gaggagacccc 120
ccccgaaata aaa 133

<210> 483
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF309964 region of
      conserved sequence in 3' untranslated region

<400> 483
atggcgtagt ggactagcggttagaggaga cccctccctt acaaatcgca gcaacaatgg 60
ggcccaagg tgagatgaag ctgttgtctc actggaagga ctagaggtta gaggagacccc 120
ccccgaaata aaa 133

<210> 484
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AF309965 region of
      conserved sequence in 3' untranslated region

<400> 484
atggcgtagt ggactagcggttagaggaga cccctccctt tcagatcgca gcaacaatgg 60
ggcccaagg tgagatgaag ctgttgtctc actggaagga ctagaggtta gaggagacccc 120
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<210> 485
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<220>
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<210> 486
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
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      conserved sequence in 3' untranslated region

<400> 486
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<210> 487
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
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      conserved sequence in 3' untranslated region

<400> 487
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<210> 488
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain AY037116 region of
      conserved sequence in 3' untranslated region

<400> 488
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<210> 489
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<212> DNA
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<220>  
<223> Dengue virus type 2 strain M19197 region of  
conserved sequence in 3' untranslated region

<400> 489  
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<210> 490  
<211> 133  
<212> DNA  
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conserved sequence in 3' untranslated region

<400> 490  
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<210> 491  
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<212> DNA  
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<220>  
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conserved sequence in 3' untranslated region

<400> 491  
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<210> 492  
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<212> DNA  
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<220>  
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conserved sequence in 3' untranslated region

<400> 492  
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<210> 493  
<211> 133  
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<220>  
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conserved sequence in 3' untranslated region

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 cccccgaaaca aaa 133

<210> 494  
 <211> 133  
 <212> DNA  
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<220>  
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 conserved sequence in 3' untranslated region

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 cccccgaaaca gaa 133

<210> 495  
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 <212> DNA  
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 conserved sequence in 3' untranslated region

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<210> 496  
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<210> 497  
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<220>  
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<210> 498
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<212> DNA
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ccccgaaaca aaa 133

<210> 499
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<212> DNA
<213> Dengue virus type 2

<220>
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ccccgaaaca aaa 133

<210> 500
<211> 133
<212> DNA
<213> Dengue virus type 2

<220>
<223> Dengue virus type 2 strain VR345-2 region of
      conserved sequence in 3' untranslated region

<400> 500
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ggcccaagg cgagatgaag ctgtgtccc gctggaagga ctagaggtta gaggagaccc 120
ccccgaaaca aaa 133

<210> 501
<211> 130
<212> DNA
<213> Dengue virus type 3

<220>
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<400> 501
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<210> 502
<211> 130
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<220>  
<223> Dengue virus type 3 strain M93130 region of  
conserved sequence in 3' untranslated region

<400> 502  
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<210> 503  
<211> 130  
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<220>  
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conserved sequence in 3' untranslated region

<400> 503  
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cggaaaacaaa 130

<210> 504  
<211> 130  
<212> DNA  
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<220>  
<223> Dengue virus type 3 strain AY099336 region of  
conserved sequence in 3' untranslated region

<400> 504  
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cggaaaataaa 130

<210> 505  
<211> 130  
<212> DNA  
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<220>  
<223> Dengue virus type 3 strain AY099337 region of  
conserved sequence in 3' untranslated region

<400> 505  
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cggaaaataaa 130

<210> 506  
<211> 130  
<212> DNA  
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<220>  
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conserved sequence in 3' untranslated region

<400> 506  
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cgcaaataaa 130

<210> 507  
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<212> DNA  
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<220>  
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conserved sequence in 3' untranslated region

<400> 507  
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<210> 508  
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conserved sequence in 3' untranslated region

<400> 508  
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cgcaaataaa 130

<210> 509  
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<212> DNA  
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conserved sequence in 3' untranslated region

<400> 509  
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cgcaaataaa 130

<210> 510  
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<212> DNA  
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<220>  
<223> Dengue virus type 3 strain AY099347 region of  
conserved sequence in 3' untranslated region

<400> 510  
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cgcaaataaa 130

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<210> 511
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<212> DNA
<213> Dengue virus type 3

<220>
<223> Dengue virus type 3 strain VR1256-3 region of
      conserved sequence in 3' untranslated region

<400> 511
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cgcaaacaaa 130

<210> 512
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<212> DNA
<213> Dengue virus type 3

<220>
<223> Dengue virus type 3 strain VR1256-5 region of
      conserved sequence in 3' untranslated region

<400> 512
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cgcaaacaaa 130

<210> 513
<211> 135
<212> DNA
<213> Dengue virus type 4

<220>
<223> Dengue virus type 4 strain M14931 region of
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accccccacaa caca 135

<210> 514
<211> 138
<212> DNA
<213> Dengue virus type 4

<220>
<223> Dengue virus type 4 strain AF289029 region of
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<400> 514
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aaagggggcc cgaaggccagg aggaagctgt actctggta gaaggactag aggttagagg 120
agacccccc aacacaaa 138

<210> 515
<211> 104
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<220>
<223> Dengue virus type 4 strain AF310150 region of
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<400> 515
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<210> 516
<211> 104
<212> DNA
<213> Dengue virus type 4

<220>
<223> Dengue virus type 4 strain AF310152 region of
      conserved sequence in 3' untranslated region

<400> 516
gtggcatatt ggactagtgg ttagaggaga cccctccat tatcaacaaa cgcagcacaa 60
        agggggcccg aagttaggat gaagctgtac tcctgtatgga agga           104

<210> 517
<211> 136
<212> DNA
<213> Dengue virus type 4

<220>
<223> Dengue virus type 4 strain AF310153 region of
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        accccccccaa cacaaa                           136

<210> 518
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<212> DNA
<213> Dengue virus type 4

<220>
<223> Dengue virus type 4 strain AF326573 region of
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<400> 518
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        accccccccaa cacaaa                           136

<210> 519
<211> 136
<212> DNA
<213> Dengue virus type 4

<220>
<223> Dengue virus type 4 strain AF326825 region of
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<400> 519
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<210> 520  
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 <212> DNA  
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<220>  
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<400> 520  
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<210> 521  
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 <212> DNA  
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<220>  
 <223> Dengue virus type 4 strain AF326827 region of  
 conserved sequence in 3' untranslated region

<400> 521  
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 agggggccca agactagagg ttagaggaga cccccc当地 acaaa 105

<210> 522  
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 <212> DNA  
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<220>  
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 conserved sequence in 3' untranslated region

<400> 522  
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 accccccc当地 cacaaa 136

<210> 523  
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<220>  
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<210> 524  
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<220>  
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<210> 525  
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conserved sequence in 3' untranslated region

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accccccaca cacaaa 136

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accccccaca cacaaa 136

<210> 527  
<211> 136  
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<220>  
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conserved sequence in 3' untranslated region

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accccccaca cacaaa 136

<210> 528  
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<212> DNA  
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<220>  
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conserved sequence in 3' untranslated region

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accccccaca 136

<210> 529
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<220>
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accccccaca 136

<210> 530
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<220>
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accccccaca 136

<210> 531
<211> 136
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<220>
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accccccaca 136

<210> 532
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<220>
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<210> 533
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<210> 534
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<212> DNA
<213> Dengue virus type 4

<220>
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accccccaca 136
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<210> 535
<211> 136
<212> DNA
<213> Dengue virus type 4

<220>
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accccccaca cacaaa

<210> 536
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<212> DNA
<213> Dengue virus type 4

<220>
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<210> 537
<211> 136
<212> DNA
<213> Dengue virus type 4

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<220>  
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conserved sequence in 3' untranslated region

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accccccaca cacaaa 136

<210> 538  
<211> 136  
<212> DNA  
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<220>  
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conserved sequence in 3' untranslated region

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accccccaca cacaaa 136

<210> 539  
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<220>  
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conserved sequence in 3' untranslated region

<400> 539  
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<220>  
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accccccaca cacaaa 136

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<220>
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<210> 545
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accccccaca cacaaa 136

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<210> 546  
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conserved sequence in 3' untranslated region

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<210> 547  
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<210> 548  
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<210> 549  
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conserved sequence in 3' untranslated region

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<210> 550  
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conserved sequence in 3' untranslated region

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<210> 552  
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<210> 553  
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<210> 554  
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<210> 555
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<210> 556
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<210> 557
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accccccaca cacaaa 136

<210> 558
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<210> 559  
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<220>  
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conserved sequence in 3' untranslated region

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<210> 560  
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<220>  
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conserved sequence in 3' untranslated region

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accccccaca caca 136

<210> 561  
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<220>  
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conserved sequence in 3' untranslated region

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accccccaca caca 136

<210> 562  
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<220>  
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conserved sequence in 3' untranslated region

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accccccaca caca 136

<210> 563  
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<210> 564  
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<210> 565  
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conserved sequence in 3' untranslated region

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<210> 566  
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<210> 567  
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conserved sequence in 3' untranslated region

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accccccaca cacaaa 136

<210> 568
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<220>
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accccccaca cacaaa 136

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<210> 571
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accccccaca cacaaa 136

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<210> 573
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<210> 575
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<210> 576
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conserved sequence in 3' untranslated region

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accccccaca cacaaa 136

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<210> 580  
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<210> 583  
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<210> 584  
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<210> 585  
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accccccaca caca 136

<210> 586  
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conserved sequence in 3' untranslated region

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<210> 587  
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accccccaca caca 136

<210> 588  
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conserved sequence in 3' untranslated region

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<210> 589  
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<220>  
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conserved sequence in 3' untranslated region

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